First experience with a new customed OpenArray™ pig intestine panel: evaluation of protein sources for piglets

Universitat Autònoma de Barcelona

Author: Francesc González Solé

Faculty of Veterinary Medicine June 2018

FACULTAT DE VETERINÀRIA

Objectives

To obtain and manage the results from a new tool to evaluate intestinal health of pig based on the genetic expression quantification with OpenArray™ technology.

To determine if these results may explain the productive responses observed in piglets fed with different protein sources early after weaning.

Materials and methods

Productive performance trial

246 commercial crossing weanling piglets were distributed in 24 pens and assigned to four treatments with different protein sources:

- T1: Soybean meal (SBM)
- T2: Animal plasma
- T3: ⅓ animal plasma + ⅔ porcine hydrolyzed mucosa
- T4: ½ animal plasma + ½ porcine hydrolyzed mucosa

Piglets fed with T2 and T3 had significant better productive performance results than piglets fed T1 (*Figure 1*).

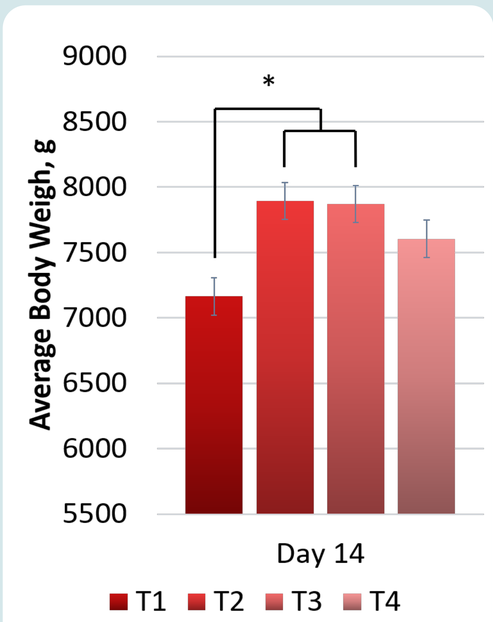

Figure 1. Average body weight of piglets on day 14 after weaning for each treatment.

OpenArray™ trial

One jejune sample per pen was collected from T1, T2 and T3. After RNA extraction, purification and reverse transcription into cDNA, gene expression was quantified with OpenArray™ technology.

OpenArray™ is an affordable real-time PCR-based solution for high-throughput gene expression analysis.

It is based on a metal plate that contains 48 subarrays with 64 through-holes each where RT-PCR take place. Every through-hole is loaded with a different gene-specific primer, a probe and 33 nL of the PCR reaction mixture.

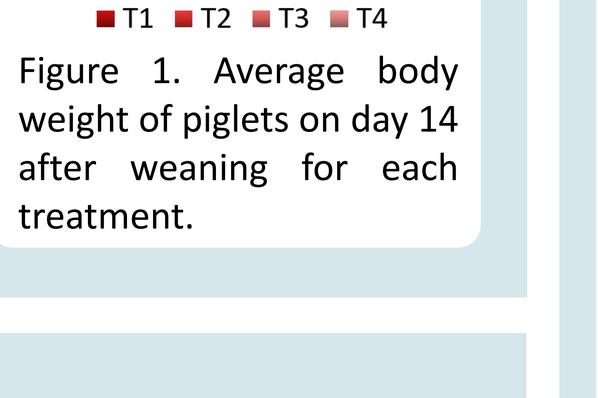

Figure 2. OpenArray™ plate

This technology minimizes the use of reagent and helps to decrease the price per data point. This way, it is possible to obtain big amounts of information at a reduced cost.

It also accelerates genomic screening as it performs 3072 RT-PCRs in just one plate.

Results

38 genes were able to be amplified and 11 of them showed significant ($p < 0.05$) or almost significant ($p < 0.1$ and > 0.05) differences.

T3 had a higher relative gene expression than T1 and T2 in most functional groups as well as in beneficial genes for intestinal health (*Figure 3*).

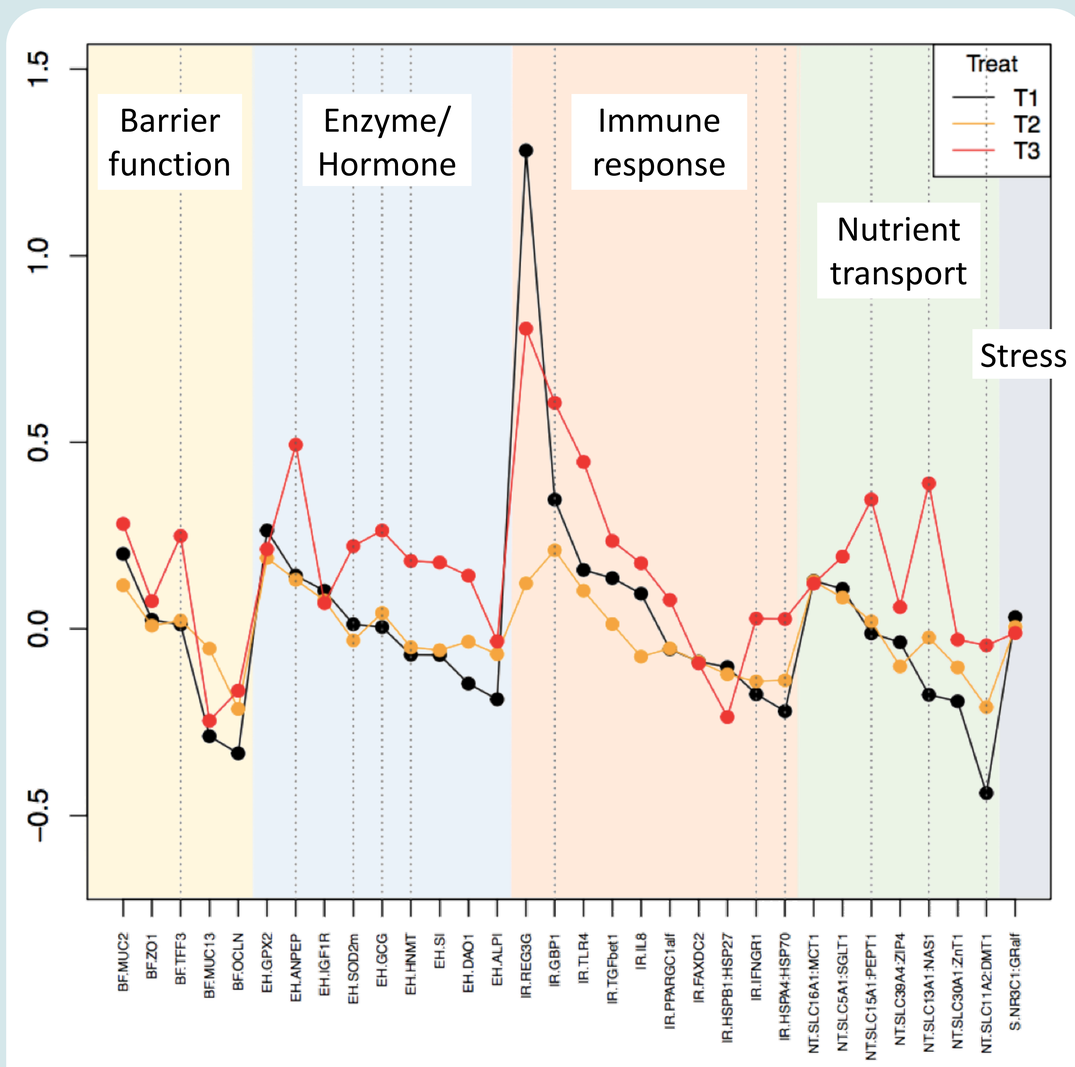

Figure 3. Relative genetic expression of each treatment for analyzed genes. Genes are organized by its functionality.

Conclusions

- ✓ Inclusion of hydrolyzed porcine mucosa increases intestinal health of weanling piglets compared to a high SBM inclusion diet and a partial replacement of SBM by animal plasma diet.
- ✓ OpenArray™ panel showed a lack of sensitivity. Pre-amplification of initial c-DNA and inclusion of a bigger sample size have been suggested to fix this problem.